



## SEQUENCE LISTING

<110> CROCE, Carlo M.  
ISHII, Hideshi

<120> COMPOSITIONS, KITS, AND METHODS RELATING TO THE HUMAN FEZ1 GENE, A NOVEL TUMOR SUPPRESSOR GENE

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<212> PRT  
<213> Homo sapiens

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35 40 45  
Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60  
Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80  
Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95  
Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln

100

105

110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Tyr Gln  
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
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Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala  
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
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Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys

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Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420                    425                    430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
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Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
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Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala  
465                    470                    480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp  
485                    490                    495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Arg Ala Glu Leu Arg  
500                    505                    510

Glu Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu  
515                    520                    525

Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys  
530                    535                    540

Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu  
545                    550                    560

Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro  
565                    570                    575

Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile  
580                    585                    590

Ala Thr Glu Ile  
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Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35                    40                    45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser  
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Leu Gln Val Leu Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu  
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Ser Tyr Glu Arg Glu  
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<211> 68  
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<213> Homo sapiens

<400> 7  
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Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu Gln  
35 40 45

Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile  
50 55 60

Leu Ala Ala His  
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<212> PRT  
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<400> 8  
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Leu Gln Val Leu Arg Leu Gln Gln Asp Lys Lys Gln Leu Gln Glu Glu  
35 40 45

Ala Ala Arg Leu Met Arg Gln Arg Glu Glu Leu Glu Asp Lys Val Ala  
50 55 60

Ala Cys Gln Lys Glu  
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<212> DNA  
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<212> DNA  
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<212> DNA  
<213> Homo sapiens

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<211> 1722  
<212> DNA  
<213> Homo sapiens

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tccacacccc ccaagctcat gccttctcc aatcagctag aaatgggctc cgagaagggt 360  
gcagtgaggg ccacagcctt caagcctgtg ctgccacggt caggagccat cctgcactcc 420  
tccccggaga gtgccagcca ccagctgcac cccggccctc cagacaagcc caaggagcag 480  
gagctgaagc ctggcctgtg ctctggggcg ctgtcagact ccggccggaa ctccatgtcc 540  
agcctgccc cacacagcac cagcagcagc taccagctgg acccgcttgt cacacccgtg 600  
ggacccacaa gccgtttgg ggctccgccc cacaacatca cccagggcat cgtccctccag 660  
gacagcaaca tgatgagcct gaaggctctg tccttctcc acggaggtag caagctggc 720

cactcgaaca aggcagacaa gggcccctcg tgtgtccgct ccccatctc cacggacgag 780  
tgcagcatcc aggagctgga gcagaagctg ttggagaggg agggcgcct ccagaagctg 840  
cagcgcagct ttgaggagaa ggagcttgcc tccagcctgg cctacgagga gcggccgcgg 900  
cgctgcaggg acgagctgga gggcccgag cccaaaggcg gcaacaagct caagcaggcc 960  
tcgcagaaga gccagcgcgc gcagcaggc ctgcacctgc aggtactgca gcttcagcag 1020  
gagaagcggc agctccggca ggagctcgag agcctcatga aggagcagga cctgctggag 1080  
accaagctca ggtcctacga gagggagaag accagctcg gccccgcgc ggaggagacc 1140  
cagtgggagg tgtgccagaa gtcagggcag atctccctcc tgaaggcagca gctgaaggag 1200  
tcccagacgg aggtgaacgc caaggcttagc gagatcctgg gtctcaaggc acagctgaag 1260  
gacacgcggc gcaagctgga gggcctggag ctgaggaccc aggacctgga gggcgcctg 1320  
cgcaccaagg gcctggagct ggaggtctgt gagaatgagc tgcaagcgc aaagaacgag 1380  
gcggagctgc tgccggagaa ggtgaacctg ctggagcagg agctgcagga gctgcggcc 1440  
caggccgccc tggcccgcga catggggccg cccaccttcc ccgaggacgt ccctgcctg 1500  
cagcgggagc tggagcggct cgtgtggaaag gaggagaagg agaaggtgat tcagtaccag 1560  
aaacagctgc agcagagcta cgtggccatg taccagcggc accagcgcct ggagaaggcc 1620  
ctgcagcagc tggcacgtgg ggacagcgc gggagccct tggaggttga cctggaagggg 1680  
gctgacatcc cctacgagga catcatagcc actgagatct ga 1722

<210> 15  
<211> 76  
<212> PRT  
<213> Homo sapiens

<400> 15  
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ala Met Thr Arg Cys Pro Arg Ala Ser Ser  
50 55 60

Met Ser Gly Ser Cys Gly Arg Arg Arg Arg Arg  
65 70 75

<210> 16  
<211> 210  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp

50

55

60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Ala Gly Glu Pro Leu Glu  
180 185 190

Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr  
195 200 205

Glu Ile  
210

<210> 17  
<211> 537  
<212> PRT  
<213> Homo sapiens

<400> 17  
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Tyr Gln  
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Asn Lys Leu Lys Gln Ala  
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
450 455 460

Arg Glu Lys His Glu Arg Leu Val Trp Lys Glu Glu Lys Glu Lys Val  
465 470 475 480

Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln  
485 490 495

Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp  
500 505 510

Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro  
515 520 525

Tyr Glu Asp Ile Ile Ala Thr Glu Ile  
530 535

<210> 18  
<211> 504  
<212> PRT  
<213> Homo sapiens

<400> 18  
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Tyr Gln  
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Asn Lys Leu Lys Gln Ala  
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg  
450 455 460

Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser  
465 470 475 480

Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr  
485 490 495

Glu Asp Ile Ile Ala Thr Glu Ile  
500

<210> 19  
<211> 563  
<212> PRT  
<213> Homo sapiens

<400> 19  
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Tyr Gln

180

185

190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Gly Asn Lys Leu Lys Gln Ala  
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
450 455 460

Arg Glu Lys Val Asn Leu Leu Glu Arg Leu Arg Ala Glu Leu Arg Glu  
465 470 475 480

Glu Arg Gln Gly His Asp Gln Met Ser Ser Gly Phe Gln His Glu Arg

485

490

495

Leu Val Trp Lys Glu Glu Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln  
500 505 510

Leu Gln Gln Ser Tyr Val Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu  
515 520 525

Lys Ala Leu Gln Gln Leu Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu  
530 535 540

Glu Val Asp Leu Glu Gly Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala  
545 550 555 560

Thr Glu Ile

<210> 20  
<211> 573  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Gly Ser Val Ser Ser Leu Ile Ser Gly His Ser Phe His Ser Lys  
1 5 10 15

His Cys Arg Ala Ser Gln Tyr Lys Leu Arg Lys Ser Ser His Leu Lys  
20 25 30

Lys Leu Asn Arg Tyr Ser Asp Gly Leu Leu Arg Phe Gly Phe Ser Gln  
35 40 45

Asp Ser Gly His Gly Lys Ser Ser Ser Lys Met Gly Lys Ser Glu Asp  
50 55 60

Phe Phe Tyr Ile Lys Val Ser Gln Lys Ala Arg Gly Ser His His Pro  
65 70 75 80

Asp Tyr Thr Ala Leu Ser Ser Gly Asp Leu Gly Gly Gln Ala Gly Val  
85 90 95

Asp Phe Asp Pro Ser Thr Pro Pro Lys Leu Met Pro Phe Ser Asn Gln  
100 105 110

Leu Glu Met Gly Ser Glu Lys Gly Ala Val Arg Pro Thr Ala Phe Lys  
115 120 125

Pro Val Leu Pro Arg Ser Gly Ala Ile Leu His Ser Ser Pro Glu Ser  
130 135 140

Ala Ser His Gln Leu His Pro Ala Pro Pro Asp Lys Pro Lys Glu Gln  
145 150 155 160

Glu Leu Lys Pro Gly Leu Cys Ser Gly Ala Leu Ser Asp Ser Gly Arg  
165 170 175

Asn Ser Met Ser Ser Leu Pro Thr His Ser Thr Ser Ser Tyr Gln  
180 185 190

Leu Asp Pro Leu Val Thr Pro Val Gly Pro Thr Ser Arg Phe Gly Gly  
195 200 205

Ser Ala His Asn Ile Thr Gln Gly Ile Val Leu Gln Asp Ser Asn Met  
210 215 220

Met Ser Leu Lys Ala Leu Ser Phe Ser Asp Gly Gly Ser Lys Leu Gly  
225 230 235 240

His Ser Asn Lys Ala Asp Lys Gly Pro Ser Cys Val Arg Ser Pro Ile  
245 250 255

Ser Thr Asp Glu Cys Ser Ile Gln Glu Leu Glu Gln Lys Leu Leu Glu  
260 265 270

Arg Glu Gly Ala Leu Gln Lys Leu Gln Arg Ser Phe Glu Glu Lys Glu  
275 280 285

Leu Ala Ser Ser Leu Ala Tyr Glu Glu Arg Pro Arg Arg Cys Arg Asp  
290 295 300

Glu Leu Glu Gly Pro Glu Pro Lys Gly Asn Lys Leu Lys Gln Ala  
305 310 315 320

Ser Gln Lys Ser Gln Arg Ala Gln Gln Val Leu His Leu Gln Val Leu  
325 330 335

Gln Leu Gln Gln Glu Lys Arg Gln Leu Arg Gln Glu Leu Glu Ser Leu  
340 345 350

Met Lys Glu Gln Asp Leu Leu Glu Thr Lys Leu Arg Ser Tyr Glu Arg  
355 360 365

Glu Lys Thr Ser Phe Gly Pro Ala Leu Glu Glu Thr Gln Trp Glu Val  
370 375 380

Cys Gln Lys Ser Gly Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Glu  
385 390 395 400

Ser Gln Thr Glu Val Asn Ala Lys Ala Ser Glu Ile Leu Gly Leu Lys  
405 410 415

Ala Gln Leu Lys Asp Thr Arg Gly Lys Leu Glu Gly Leu Glu Leu Arg  
420 425 430

Thr Gln Asp Leu Glu Gly Ala Leu Arg Thr Lys Gly Leu Glu Leu Glu  
435 440 445

Val Cys Glu Asn Glu Leu Gln Arg Lys Lys Asn Glu Ala Glu Leu Leu  
450 455 460

Arg Glu Lys Val Asn Leu Leu Glu Gln Glu Leu Gln Glu Leu Arg Ala  
465 470 475 480

Gln Ala Ala Leu Ala Arg Asp Met Gly Pro Pro Thr Phe Pro Glu Asp  
485 490 495

Val Pro Ala Leu Gln Arg Glu Leu Glu Arg Leu Val Trp Lys Glu Glu  
500 505 510

Lys Glu Lys Val Ile Gln Tyr Gln Lys Gln Leu Gln Gln Ser Tyr Val  
515 520 525

Ala Met Tyr Gln Arg Asn Gln Arg Leu Glu Lys Ala Leu Gln Gln Leu  
530 535 540

Ala Arg Gly Asp Ser Ala Gly Glu Pro Leu Glu Val Asp Leu Glu Gly  
545 550 555 560

Ala Asp Ile Pro Tyr Glu Asp Ile Ile Ala Thr Glu Ile  
565 570

<210> 21  
<211> 591  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: F37 Probe

<400> 21  
ggactctgcc cctggacactg ggaacgactg gactgtcacg gggttccctc ctagctctcc 60  
cagtgaaactc ctgccaggca cacacagccc ctatagcact gagctcacat gggactggga 120  
tatggggca tcttcccc agagaggcac tcagttagcc tcctgtgcct ggccccagtc 180  
tggccatct cttaggtgag acagttgccc gaaactaagc caggcctggc tggaggagca 240  
gcagcttggg gagagggatt tccctgcaga cctcaagcca tcatgcgttg ggtgctgcca 300  
tgacagaggc tgcaccctg ggccagcggg gctgctcacc cacctttgt gcaagggtggc 360  
ctttgtctg cgccctgcagg cagagctgga gccccagca gaggcaggct gggacggacc 420  
agcatctgga agatgtacat agttatttt ctctttgtgg tttcttgttt ggtttgggtt 480  
gctttgaca gcttcatttt attttgacg tcactttttg gccatgtaaa ctatttgtgg 540  
caattttatg ttttattta tgaataaaga atgccatttc tcacgccctc t 591

<210> 22  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplificatin primer G12

<400> 22  
gctgccacag cctttccaag acc

23

<210> 23  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplificatin primer G13

<400> 23  
taccgggtga gcttcttgag gtg

23

<210> 24  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G14.2

<400> 24  
acagcttcca cagcaaggcac tgc

23

<210> 25  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G15

<400> 25  
attggagaag ggcatgagct t

21

<210> 26  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G16

<400> 26  
tggactttga cccgtccaca cc

22

<210> 27  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntABR

<400> 27  
gttccaacc cacttacct tgc 23

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntABF

<400> 28  
gcaggggagg catgagtcac c 21

<210> 29  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G17

<400> 29  
ggttcagct cctgctccctt gg 22

<210> 30  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G20

<400> 30  
acaacatcac ccagggcatc gtc 23

<210> 31  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G21

<400> 31  
cctccagtc gtccctgcag c 21

<210> 32

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G32

<400> 32  
actgcagctt cagcaggaga agc 23

<210> 33  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntBCR

<400> 33  
ctgaccaccc aaacccatga gc 22

<210> 34  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer IntBCF

<400> 34  
tcacctcttg gcactctgtc tcc 23

<210> 35  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer Mut6

<400> 35  
caggtcctgg gtcctcagct c 21

<210> 36  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G1

<400> 36  
tgaacgccaa ggcttagcgag atc

23

<210> 37  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G2

<400> 37  
gctcctgcag ctcctgctcc ag

22

<210> 38  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G75

<400> 38  
cccaccttcc ccgaggacgt c

21

<210> 39  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G82

<400> 39  
agccccgagga catctggtca tgg

23

<210> 40  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G5

<400> 40  
cctgccctgc agcgggagct ggag

24

<210> 41  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G6

<400> 41  
agctgctgca gggccttctc cag 23

<210> 42  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G7

<400> 42  
cagtaccaga aacagctgca gcagagc 27

<210> 43  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: FEZ1 alterable  
region amplification primer G8

<400> 43  
ccctgcctcc cagtgccagg tc 22

<210> 44  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: First strand  
of partially-double stranded adapter-linker

<400> 44  
gatctcgacg aattcgtag acct 24

<210> 45  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Second strand  
of partially-double stranded adapter-linker

<400> 45  
tggtctcacg aattcgtcga 20

<210> 46  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

<400> 46  
tcccaggact ccggcacgg caa 23

<210> 47  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 47  
gagcgcaag gccatgacca g 21

<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

<400> 48  
agcctgcccc cacacagcac cag 23

<210> 49  
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 49  
cagcgccggg gagcccttgg a 21

<210> 50  
<211> 23  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Donor site sequence of truncated FEZ1 truncation region

<400> 50  
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<210> 51  
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<223> Description of Artificial Sequence: Acceptor site sequence of truncated FEZ1 truncation region

<400> 51  
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<210> 52  
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<223> Description of Artificial Sequence: Donor site sequence of truncated FEZ1 truncation region

<400> 52  
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<210> 53  
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<223> Description of Artificial Sequence: Acceptor site sequence of truncated FEZ1 truncation region

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<210> 54  
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sequence of truncated FEZ1 truncation region

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<210> 55  
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<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

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<210> 56  
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<212> DNA  
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<223> Description of Artificial Sequence: Donor site  
sequence of truncated FEZ1 truncation region

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<210> 57  
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<212> DNA  
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<223> Description of Artificial Sequence: Acceptor site  
sequence of truncated FEZ1 truncation region

<400> 57  
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<210> 58  
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<223> Description of Artificial Sequence: Primer for  
amplifying FEZ1 cDNA

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27

<210> 59  
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<212> DNA  
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<223> Description of Artificial Sequence: Primer for  
amplifying FEZ1 cDNA

<400> 59  
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<210> 60  
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<223> Description of Artificial Sequence: Example

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<223> Description of Artificial Sequence: Example

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<223> Description of Artificial Sequence: Example

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<223> Description of Artificial Sequence: Example

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